

Carboxy terminus
of α -factor:

Gly — Gln -- Pro -- Met -- Tyr COOH

Possible codons
and their usage

GGU (90)	CAA (20)	CCA (32)	AUG (20)	UAC (33)
GGC (3)	CAG (0)	CCU (3)		UAU (0)
GGA (0)		CCC (1)		
GGG (0)		CCG (0)		

Consensus
oligonucleotides:

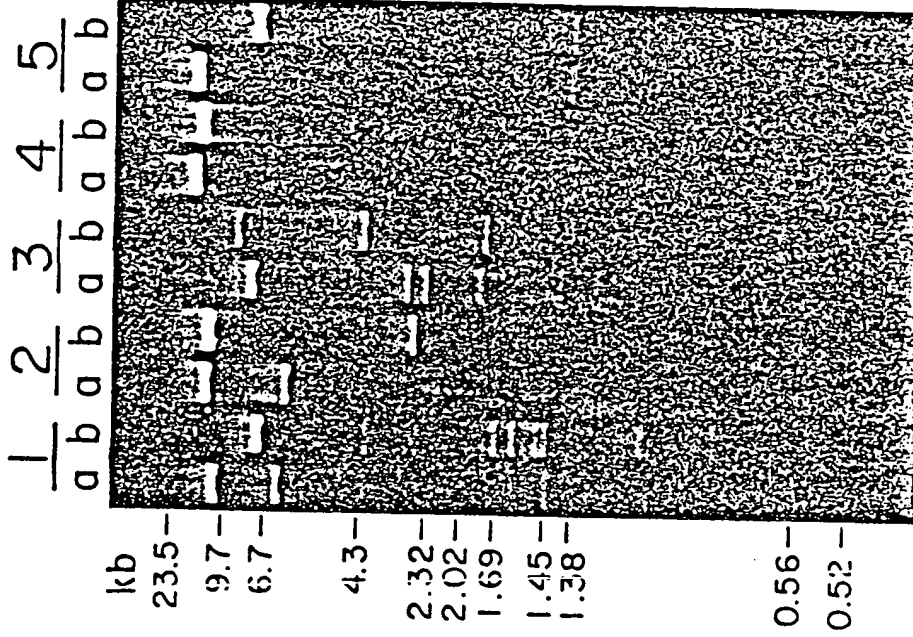
5'-GG^T_CCAACC^A_TATGTAC

Synthesized
oligonucleotide
pools complemen-
tary to above:

I. 5'-GTACATTGGTTG^A_GCC
II. 5'-GTACATAGGTTG^A_GCC

FIGURE 1

A



B

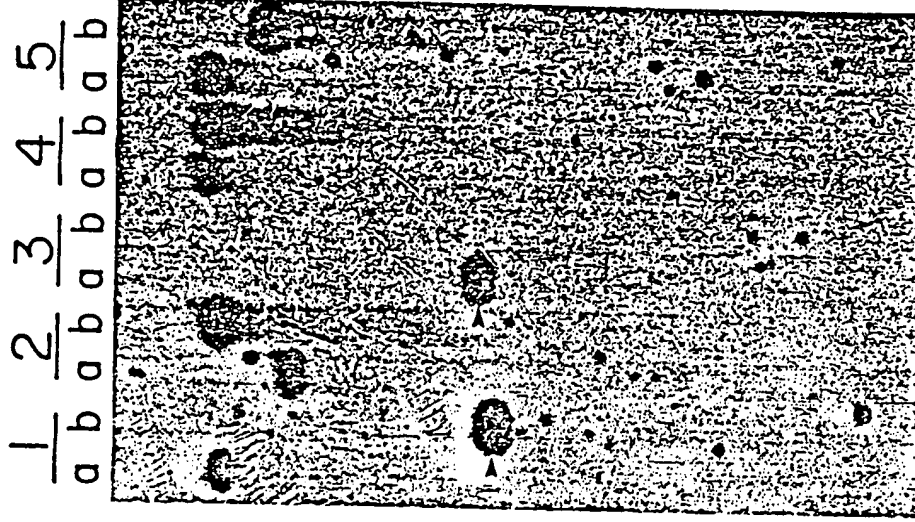


FIGURE 2

CGACAGTAAATTTGCCGAATTTAATAGCTTCTACTGAAAAACAGTGGACCATGTGAAAAGATGCATCTCATTATCAA
 -280 -260 -240 -220
 ACACATAATATTCAAGTGAGCCTTACTTCAATTGTATTGAAGTGCAAGAAAACCAAAAAGCAACAGGTTTGGATA
 -200 -180 -160 -140
 AGTACATATATAAGAGGGCCTTTTGTCCCATCAAAAATGTTACTGTTCTTACGATTTCATTACGATTCAAGAATAGTT
 -120 -100 -80 -60
 CAAACAAGAAGATTACAACTATCAATTTATACACAATATAAACGATTAAAGA ATG AGA TTT CCT TCA ATT
 -40 -20 1
 Met Arg Phe Pro Ser Ile
 Phe Thr Ala Val Leu Phe Ala Ala Ser Ser Ala Leu Ala Ala Pro Val Asn Thr Thr Thr
 TTT ACT GCA GTT TTA TTC GCA GCA TCC TCC GCA TTA GCT GCT CCA GTC AAC ACT ACA ACA
 20 40 60
 Glu Asp Glu Thr Ala Gln Ile Pro Ala Glu Ala Val Ile Gly Tyr Leu Asp Leu Glu Gly
 GAA GAT GAA ACG GCA CAA ATT CCG GCT GAA GCT GTC ATC GGT TAC TTA GAT TTA GAA GGG
 80 100 120
 Asp Phe Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu Phe Ile
 GAT TTC GAT GTT GCT GTT TTG CCA TTT TCC AAC AGC ACA AAT AAC GGG TTA TTG TTT ATA
 140 160 180
 Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val Ser Leu Asp Lys Arg Glu
 AAT ACT ACT ATT GCC AGC ATT GCT GCT AAA GAA GAA GGG GTA TCT TTG GAT AAA AGA GAG
 200 220 240
 Ala Glu Ala Trp His Trp Leu Gln Leu Lys Pro Gly Gln Pro Met Tyr Lys Arg Glu Ala
 GCT GAA GCT TGG CAT TGG TTG CAA CTA AAA CCT GGC CAA CCA ATG TAC AAG AGA GAA GCC
 260 280 300
 Glu Ala Glu Ala Trp His Trp Leu Gln Leu Lys Pro Gly Gln Pro Met Tyr Lys Arg Glu
 GAA GCT GAA GCT TGG CAT TGG CTG CAA CTA AAG CCT GGC CAA CCA ATG TAC AAA AGA GAA
 320 340 360
 Ala Asp Ala Glu Ala Trp His Trp Leu Gln Leu Lys Pro Gly Gln Pro Met Tyr Lys Arg
 GCC GAC GCT GAA GCT TGG CAT TGG CTG CAA CTA AAG CCT GGC CAA CCA ATG TAC AAA AGA
 380 400 420
 Glu Ala Asp Ala Glu Ala Trp His Trp Leu Gln Leu Lys Pro Gly Gln Pro Met Tyr End
 GAA GCC GAC GCT GAA GCT TGG CAT TGG TTG CAG TTA AAA CCC GGC CAA CCA ATG TAC TAA
 440 460 480
 GCCCGACTGATAACAACAGTGTAGATGTAACAAGTCGACTTTGTTCCCACTGTACTTTTAGCTCGTACAAAATACAAT
 500 520 540 560
 ATACTTTTCATTTCTCCGTAACAACATGTTTTCCCATGTAATATCCTTTTCTATTTTTCGTTCCGTTACCAACTTTAC
 580 600 620 640
 ACATACTTTATATAGCTATTCACCTTCTATACACTAAAAAACTAAGACAATTTTAATTTTGTGCTGCCATATTTCAAT
 660 680 700 720
 TTGTTATAAATTCCTATAATTTATCCTATTAGTAGCTAAAAAAGATGAATGTGAATCGAATCCTAAGAGAATTC
 740 760 780 800

FIGURE 3

TTCTTCATTGGTACATCAATGCCAGCAACGATGTGCGCATCTGGGCGACGCCTGTAGTGATTGTTTTCAAGGTATCGAG
 -300 -280 -260 -240
 CCAAACATATTCATCGTTACTGTTTCAAATATTCAGTTGTTTTCAGTACAGAGTCGCCGTGGACCTAGTGAAACTTGGTGT
 -220 -200 -180 -160
 CTTTACAGCGCAGAGACGAGGGCTTATATGTATAAAAGCTGTCTTGATTCTGGTGTAGTTTGAGGTGTCTTCTCTATA
 -140 -120 -100 -80
 TCTGTTTTATATTCTATATAATGGATAATTACTACCATCACCTGCATCAAATTCAGTAAATTCACATATTGGAGAAA
 -60 -40 -20
 1 10 20
 Met Lys Phe Ile Ser Thr Phe Leu Thr Phe Ile Leu Ala Ala Val Ser Val Thr Ala Ser
 ATG AAA TTC ATT TCT ACC TTT CTC ACT TTT ATT TTA GCG GCC GTT TCT GTC ACT GCT AGT
 1 20 40 60
 30 40
 Ser Asp Glu Asp Ile Ala Gln Val Pro Ala Glu Ala Ile Ile Gly Tyr Leu Asp Phe Gly
 TCC GAT GAA GAT ATC GCT CAG GTG CCA GCC GAG GCC ATT ATT GGA TAC TTG GAT TTC GGA
 80 100 120
 50 60
 Gly Asp His Asp Ile Ala Phe Leu Pro Phe Ser Asn Ala Thr Ala Ser Gly Leu Leu Phe
 GGT GAT CAT GAC ATA GCT TTT TTA CCA TTC AGT AAC GCT ACC GCC AGT GGG CTA TTG TTT
 140 160 180
 70 80
 Ile Asn Thr Thr Ile Ala Glu Ala Ala Glu Lys Glu Gln Asn Thr Thr Leu Ala Lys Arg
 ATC AAC ACC ACT ATT GCT GAG GCG GCT GAA AAA GAG CAA AAC ACC ACT TTG GCG AAA AGA
 200 220 240
 90 100
 Glu Ala Val Ala Asp Ala Trp His Trp Leu Asn Leu Arg Pro Gly Gln Pro Met Tyr Lys
 GAG GCT GTT GCC GAC GCT TGG CAC TGG TTA AAT TTG AGA CCA GGC CAA CCA ATG TAC AAG
 260 280 300
 110 120
 Arg Glu Ala Asn Ala Asp Ala Trp His Trp Leu Gln Leu Lys Pro Gly Gln Pro Met Tyr
 AGA GAG GCC AAC GCT GAT GCT TGG CAC TGG TTG CAA CTC AAG CCA GGC CAA CCA ATG TAC
 320 340 360
 End
 TGA AAAATGACCCTAAACTACTTCTAAACCCTCTCGATTCTTTTACGTTTCATACAACACCTAGTTTTATTATTTTC
 380 400 420
 TTTTCAATCTGAGTAGTTGAGTTTTCGATCACTCACATAGAACTATTTTTGCCATTAAATAAAGTATTCTCTCAAAT
 440 460 480 500
 GATGCGATACTATAATACTCTTTGCCATATATTACATTCATTATAAATAGGCTATGTTTCTATATCCGTTTCCGATTC
 520 540 560 580
 TGTCTGCAAGCAAGGTTCCCTATCATTACCGGATTGTTCACTATGGTTGGAGCTC
 600 620 640

FIGURE 4

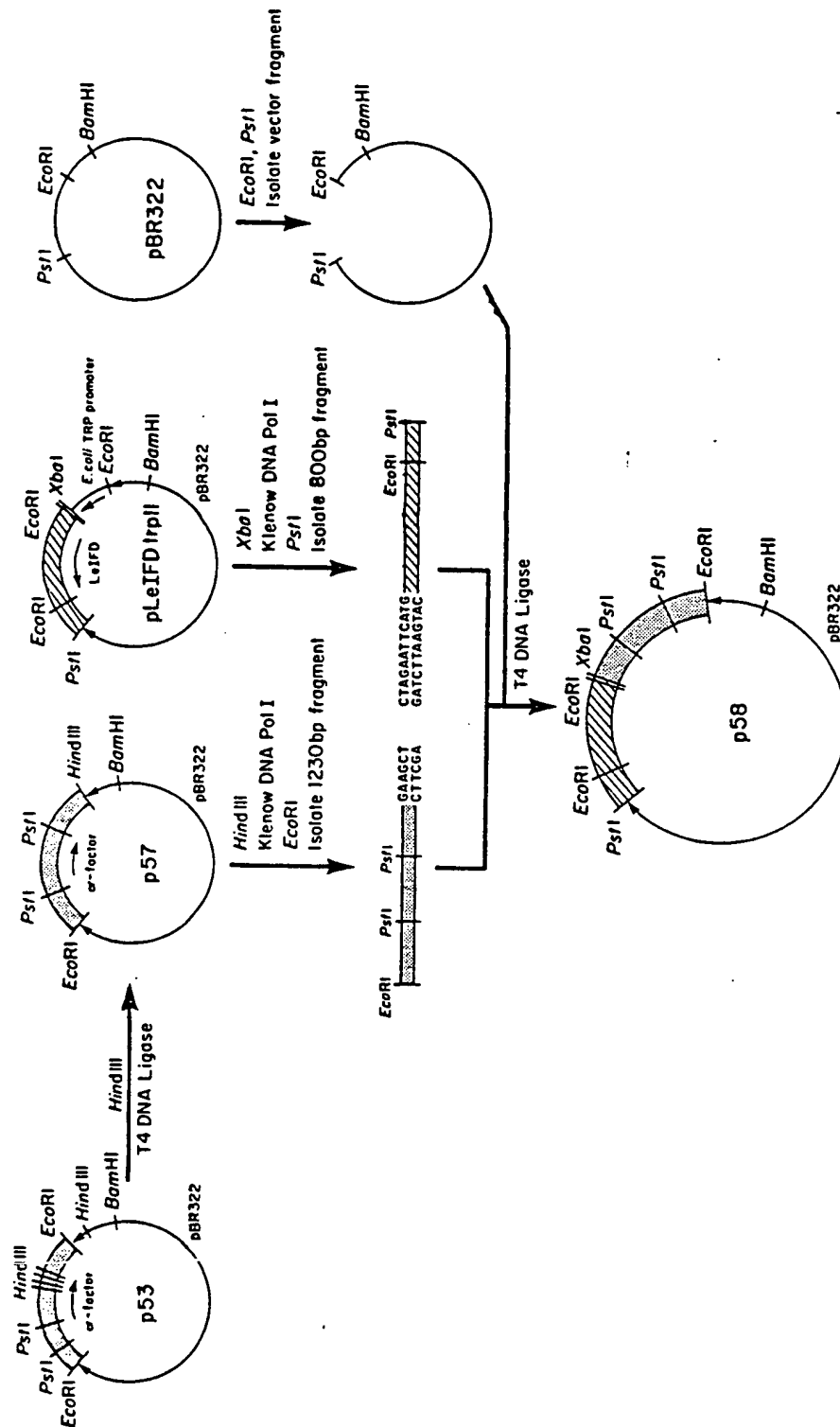


FIGURE 5

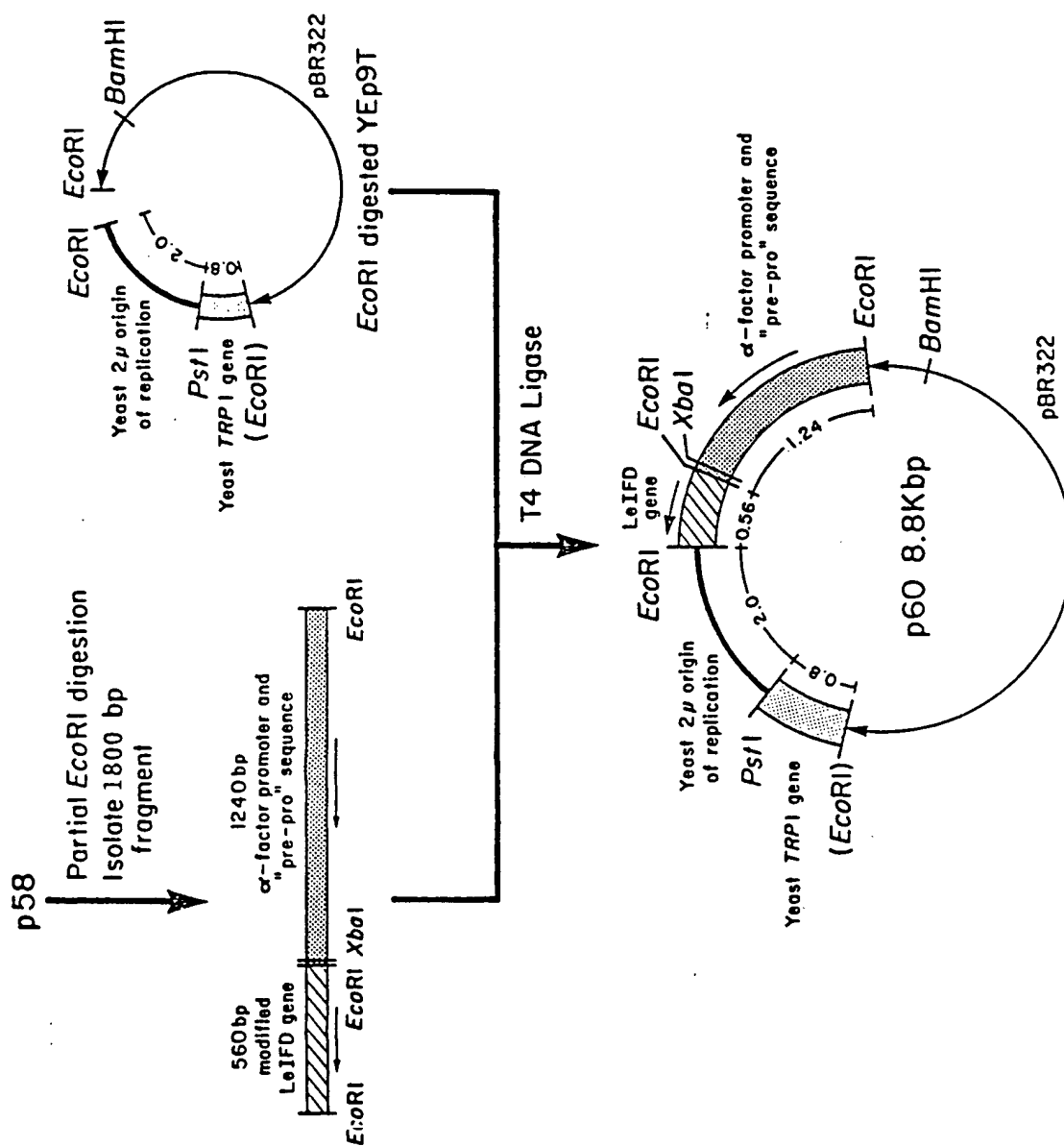


FIGURE 6

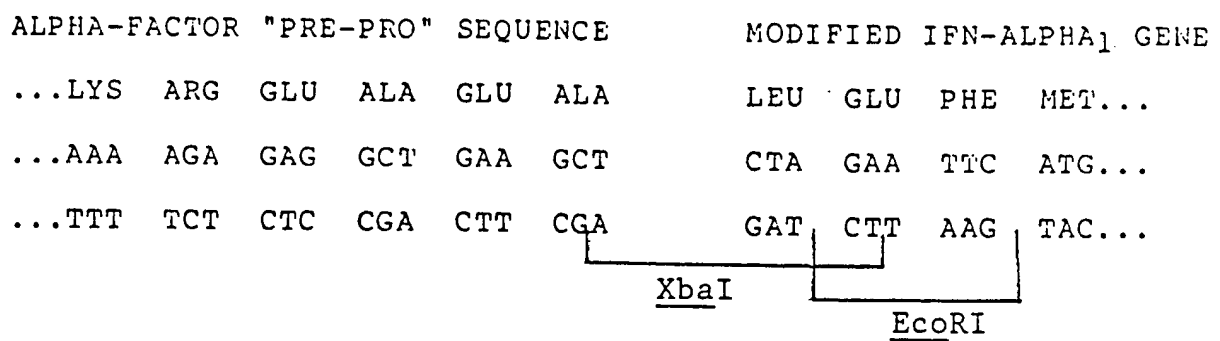


FIGURE 7

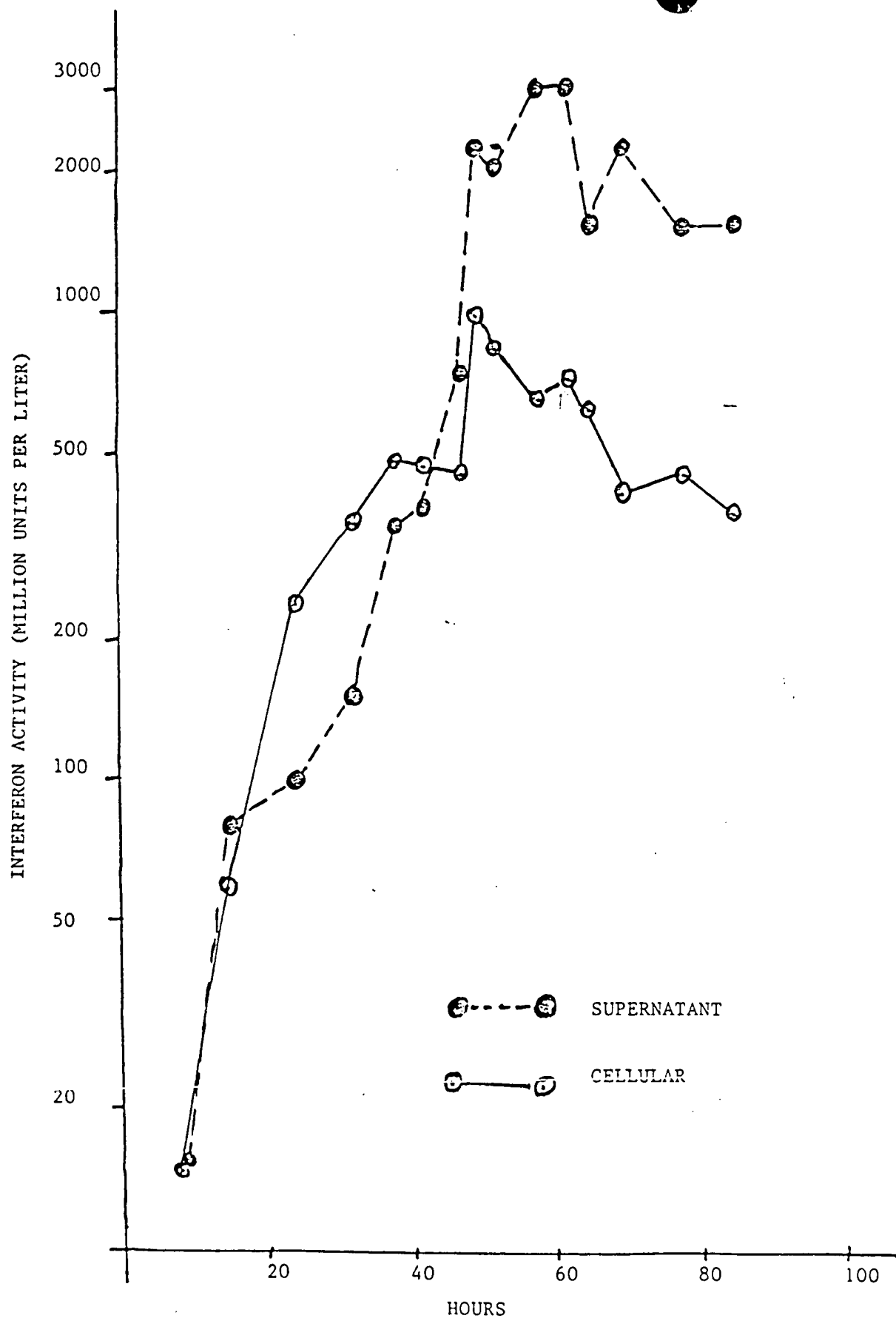


FIGURE 8

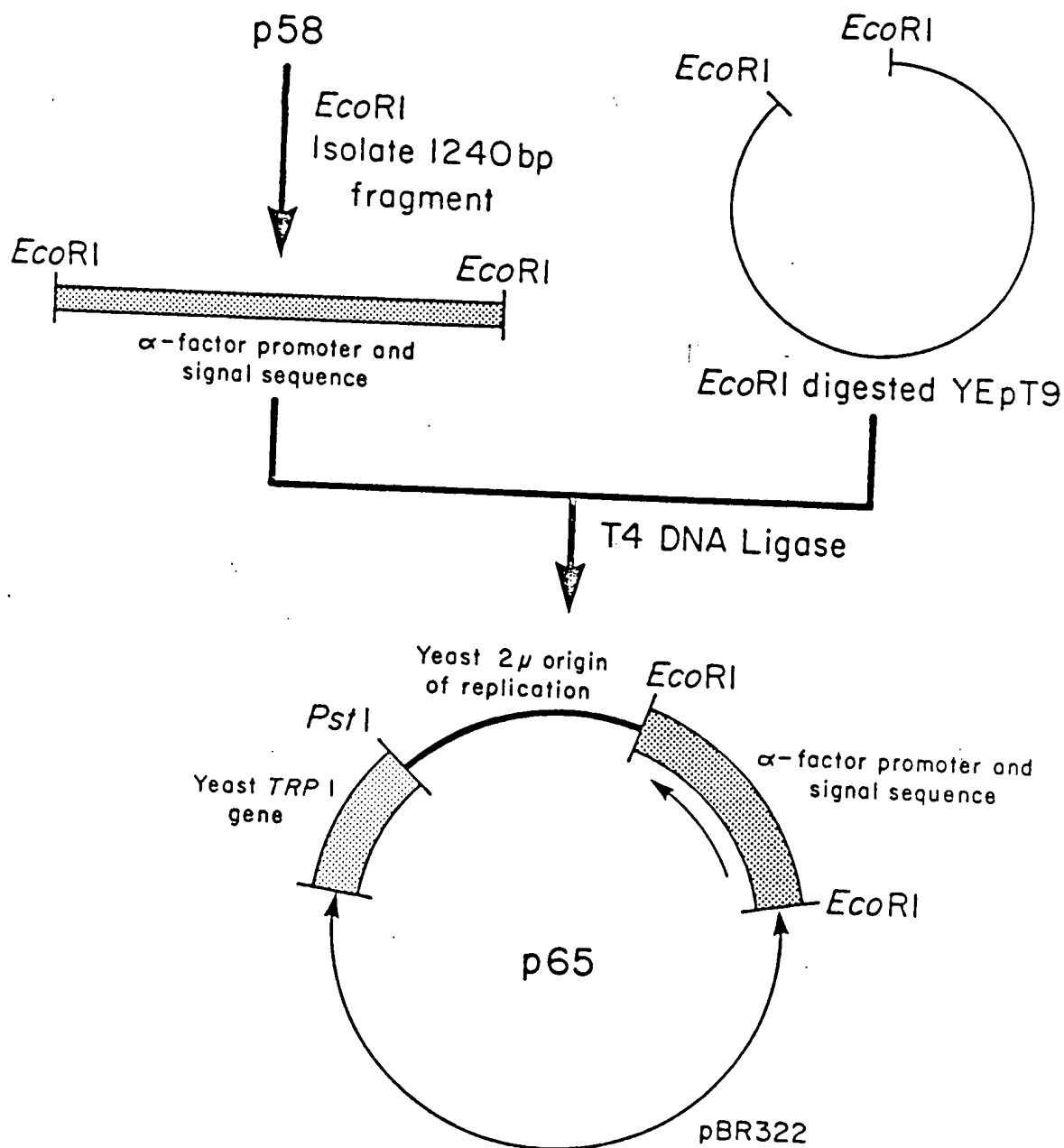


FIGURE 9

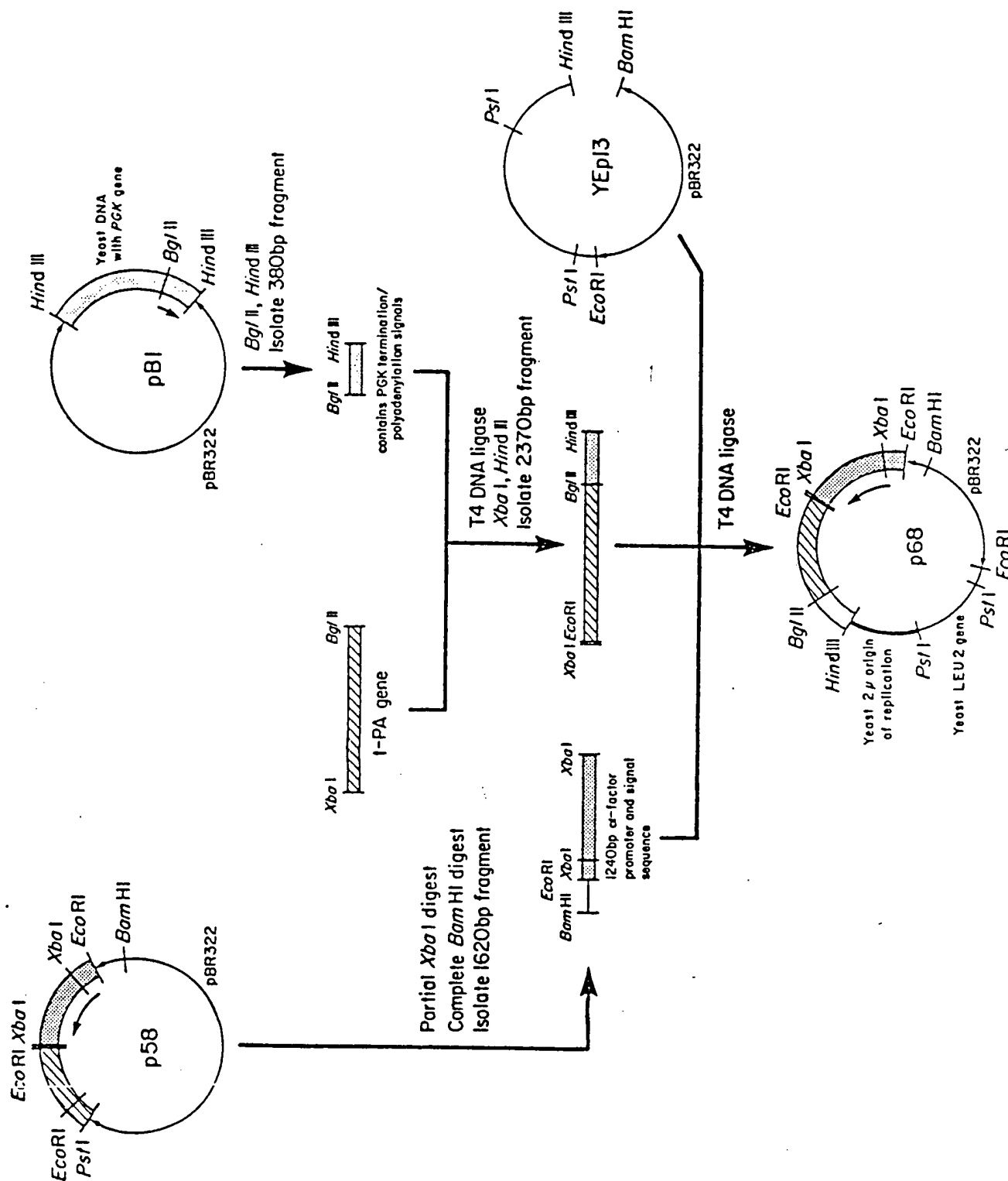


FIGURE 10

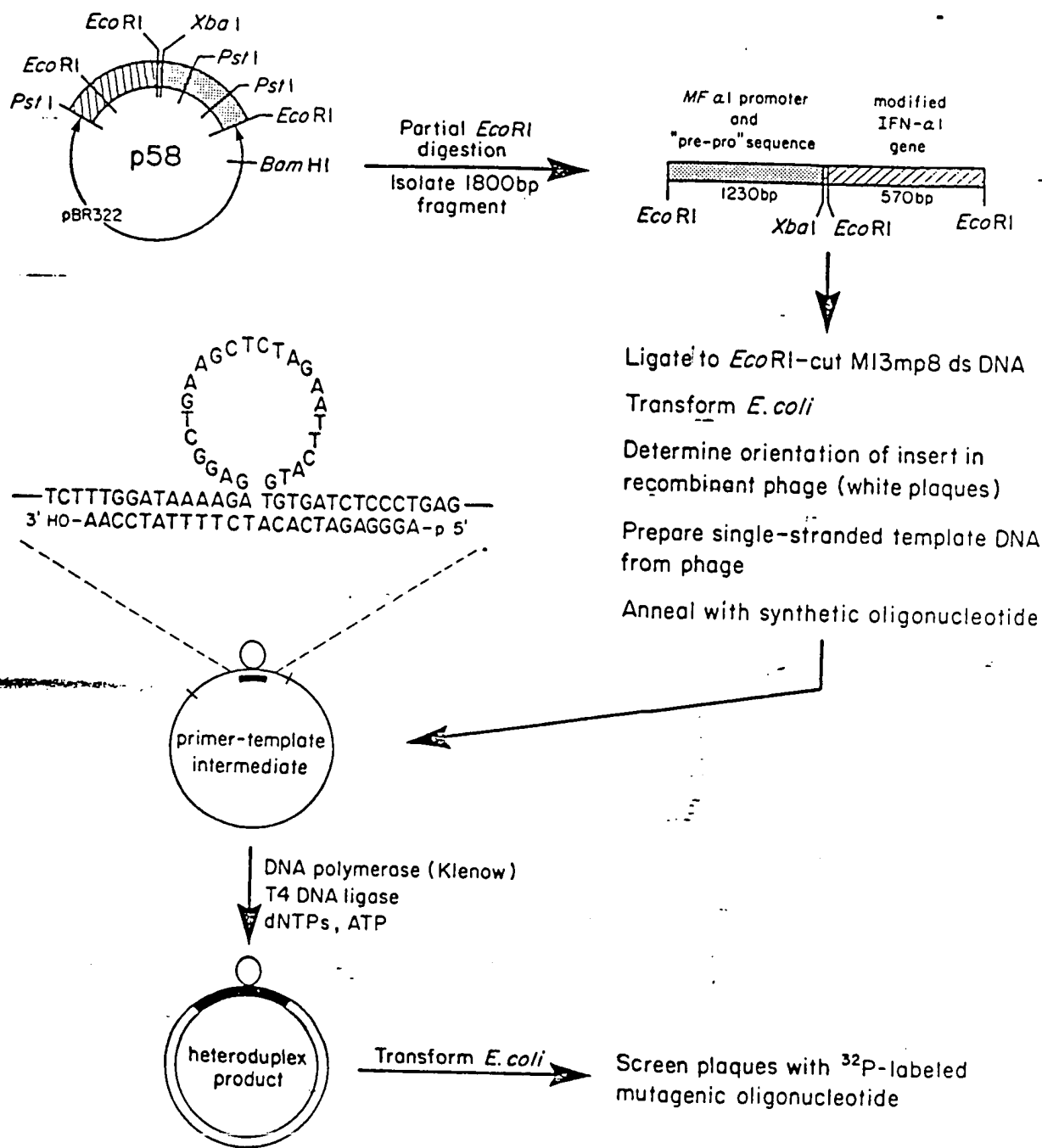


FIGURE 11

	1	10	20
MF _α 1	MetArgPheProSerIlePheThrAlaValLeuPheAlaAlaSerSerAlaLeuAlaAla		
MF _α 2	MetLysPheIleSerThrPheLeuThrPhe-----IleLeuAlaAla		
Consensus	Met---Phe---Ser---Phe-----LeuAlaAla		
	30	40	
MF _α 1	ProValAsnThr---ThrThrGluAspGluThrAlaGlnIleProAlaGluAlaValIle		
MF _α 2	ValSerValThrAlaSerSerAspGluAspIleAlaGlnValProAlaGluAlaIleIle		
Consensus	-----Thr-----AlaGln---ProAlaGluAla---Ile		
	50	60	
MF _α 1	GlyTyrLeuAspLeuGluGlyAspPheAspValAlaValLeuProPheSerAsnSerThr		
MF _α 2	GlyTyrLeuAspPheGlyGlyAspHisAspIleAlaPheLeuProPheSerAsnAlaThr		
Consensus	GlyTyrLeuAsp-----GlyAsp---Asp---Ala---LeuProPheSerAsn---Thr		
	70	80	
MF _α 1	AsnAsnGlyLeuLeuPheIleAsnThrThrIleAlaSerIleAlaAlaLysGluGluGly		
MF _α 2	AlaSerGlyLeuLeuPheIleAsnThrThrIleAlaGluAlaAlaGluLysGluGlnAsn		
Consensus	-----GlyLeuLeuPheIleAsnThrThrIleAla-----Ala---LysGlu-----		
	90	100	
MF _α 1	ValSerLeuAspLysArgGluAlaGlu-----AlaTrpHisTrpLeuGlnLeuLysPro		
MF _α 2	ThrThrLeuAlaLysArgGluAlaValAlaAspAlaTrpHisTrpLeuAsnLeuArgPro		
Consensus	-----Leu---LysArgGluAla-----AlaTrpHisTrpLeu---Leu---Pro		
	110	120	
MF _α 1	GlyGlnProMetTyrLysArgGluAlaGluAlaGluAlaTrpHisTrpLeuGlnLeuLys		
MF _α 2	GlyGlnProMetTyrLysArgGluAlaAsnAlaAspAlaTrpHisTrpLeuGlnLeuLys		
Consensus	GlyGlnProMetTyrLysArgGluAla---Ala---AlaTrpHisTrpLeuGlnLeuLys		
	130	140	
MF _α 1	ProGlyGlnProMetTyrLysArgGluAlaAspAlaGluAlaTrpHisTrpLeuGlnLeu		
MF _α 2	ProGlyGlnProMetTyr		
Consensus	ProGlyGlnProMetTyr-----		
	150	160	
MF _α 1	LysProGlyGlnProMetTyrLysArgGluAlaAspAlaGluAlaTrpHisTrpLeuGln		
Consensus	-----		
	168		
MF _α 1	LeuLysProGlyGlnProMetTyr		
Consensus	-----		

FIGURE 12